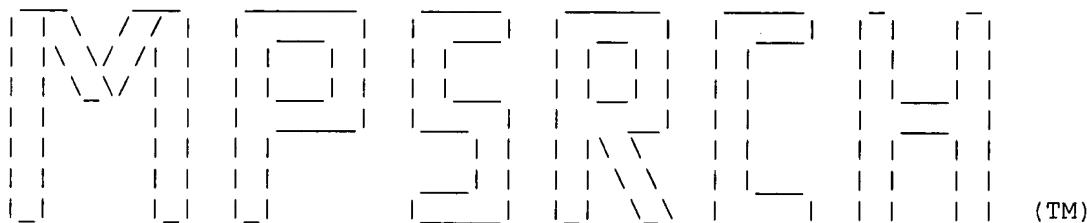


Parent

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Dec 9 17:28:12 1997; MasPar time 9.66 Seconds  
505.272 Million cell updates/sec

Tabular output not generated.

Title: :>US-08-774-104A-2  
Description: (1-397) from US08774104A.pep  
Perfect Score: 2738  
Sequence: 1 MMTYHETRALAQSDLQQLYA.....ETGLKFEPMRQLLKDYHVE 397

Scoring table: PAM 150  
Gap 11

Searched: 101610 seqs, 12294212 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: a-geneseq28  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19 20:part20 21:part21

Statistics: Mean 34.745; Variance 172.154; scale 0.202

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query					Description	Pred. No.
No.	Score	Match	Length	DB	ID		
1	185	6.8	518	2	P70506	TrpE enzyme.	2.82e-05
2	165	6.0	193	1	P80877	Hook region #8 contg	8.20e-04
3	165	6.0	225	2	P70061	Sequence of human gro	8.20e-04
4	165	6.0	225	2	P70359	Sequence encoded by p	8.20e-04

5	165	6.0	262	4	P40023	Fusion protein contg.	8.20e-04
6	165	6.0	405	4	P30202	Sequence encoded by p	8.20e-04
7	155	5.7	406	4	P30203	Sequence encoded by p	4.29e-03
8	155	5.7	609	4	P30206	Sequence encoded by p	4.29e-03
9	114	4.2	450	13	R70030	UTH1 gene product.	2.88e+00
10	111	4.1	988	2	R24302	Transposase from glyc	4.53e+00
11	106	3.9	671	3	R14548	T cell transmembrane	9.56e+00
12	106	3.9	724	10	R53468	T-cell transmembrane	9.56e+00
13	106	3.9	763	20	W08136	Human cytokine respon	9.56e+00
14	106	3.9	763	9	R49790	Sequence of special A	9.56e+00
15	102	3.7	513	13	R77860	S. clavuligerus ORF3	1.72e+01
16	101	3.7	566	21	W11217	Leishmania tropica Lt	1.99e+01
17	95	3.5	1117	10	R53146	Mouse tyrosine kinase	4.74e+01
18	95	3.5	1122	9	R48627	Protein-tyrosine-kin	4.74e+01
19	95	3.5	1123	12	R67391	Murine tyrosine kinas	4.74e+01
20	95	3.5	1123	14	R73951	Mouse tie-2 receptor	4.74e+01
21	94	3.4	242	13	R71091	C. jejuni PEB1A antig	5.46e+01
22	94	3.4	387	1	P80851	Sequence of Tritirach	5.46e+01
23	92	3.4	3135	11	R57474	P. falciparum transmi	7.25e+01
24	89	3.3	111	8	R47492	Humanised anti-CD18 A	1.10e+02
25	91	3.3	231	21	W20162	H. pylori inner membr	8.34e+01
26	91	3.3	433	19	W05196	Helicobacter pylori 5	8.34e+01
27	91	3.3	435	15	R86288	Erwinia rhabontici su	8.34e+01
28	91	3.3	438	21	W20916	H. pylori inner membr	8.34e+01
29	91	3.3	455	18	R87533	Pseudomonas aureofaci	8.34e+01
30	89	3.3	497	21	W20821	H. pylori cell envelo	1.10e+02
31	89	3.3	703	14	R76237	Human placental endot	1.10e+02
32	89	3.3	753	14	R76227	Human endothelin conv	1.10e+02
33	89	3.3	753	13	R75691	Endothelin converting	1.10e+02
34	89	3.3	758	19	W03682	Human endothelin conv	1.10e+02
35	89	3.3	758	18	W03736	Human endothelin conv	1.10e+02
36	91	3.3	1124	14	R73953	Human TEK tyrosine ki	8.34e+01
37	91	3.3	1124	9	R45440	Human orphan receptor	8.34e+01
38	90	3.3	2035	11	R57141	Host cell factor prot	9.59e+01
39	88	3.2	387	18	R87534	Pseudomonas aureofaci	1.27e+02
40	87	3.2	600	15	R86290	Protaminobacter rubru	1.45e+02
41	88	3.2	687	1	P81152	Herbicide sensitive,	1.27e+02
42	88	3.2	1290	15	R90583	Phospholipase C-gamma	1.27e+02
43	87	3.2	1522	2	P93357	Sequence of the catal	1.45e+02
44	87	3.2	1705	2	P94365	Sequence of part of a	1.45e+02
45	87	3.2	1706	2	R08031	Adenyl cyclase from B	1.45e+02

#### ALIGNMENTS

RESULT 1

ID P70506 standard; protein; 518 AA.

AC P70506;

DT 11-JAN-1991 (first entry)

DE TrpE enzyme.

KW L-Tryptophan; TrpE; amino acid.

PN J62244382-A.

PD 24-OCT-1987.

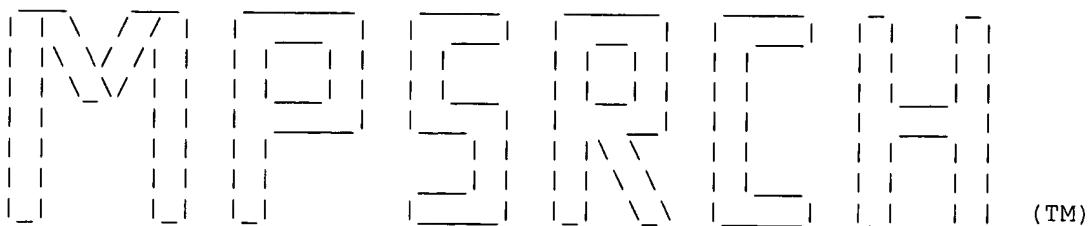
PF 16-APR-1986; 087600.

PR 16-APR-1987; JP-087600.

PA (AJIN ) AJINOMOTO KK.

DR WPI; 87-339035/48.

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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Dec 9 17:30:10 1997; MasPar time 10.34 Seconds  
814.531 Million cell updates/sec

Tabular output not generated.

Title: >US-08-774-104A-2  
Description: (1-397) from US08774104A.pep  
Perfect Score: 2738  
Sequence: 1 MMTYHETRALAQSDLQQLYA.....ETGLKFEPMRQLLKDYNHVE 397

Scoring table: PAM 150  
Gap 11

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: swiss-prot34  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 50.794; Variance 108.721; scale 0.467

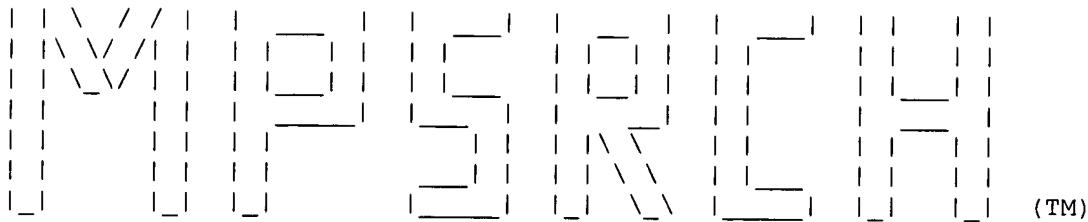
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result	Query	No.	Score	Match	Length	DB	ID	Description	Pred. No.
<hr/>									
1	624	22.8	471	6	MENF_BACSU	MENAQUINONE-SPECIFIC		1.50e-88	
2	457	16.7	391	3	ENTC_ECOLI	ISOCHORISMATE SYNTHAS		9.99e-58	
3	434	15.9	396	1	AMOA_AERHY	PUTATIVE ISOCHORISMAT		1.44e-53	
4	429	15.7	431	6	MENF_ECOLI	MENAQUINONE-SPECIFIC		1.15e-52	
5	400	14.6	398	3	DHBC_BACSU	ISOCHORISMATE SYNTHAS		1.81e-47	
6	380	13.9	430	6	MENF_HAEIN	MENAQUINONE-SPECIFIC		6.48e-44	
7	372	13.6	523	9	TRPE_HALVO	ANTHRANILATE SYNTHASE		1.68e-42	

8	364	13.3	456	9	TRPE_LACLA	ANTHRANILATE SYNTHASE	4.33e-41
9	361	13.2	421	9	TRPE_SULSO	ANTHRANILATE SYNTHASE	1.46e-40
10	360	13.1	470	7	PABB_BACSU	PARA-AMINOBENZOATE SY	2.19e-40
11	337	12.3	512	9	TRPE_BACPU	ANTHRANILATE SYNTHASE	2.29e-36
12	328	12.0	515	9	TRPE_BACSU	ANTHRANILATE SYNTHASE	8.32e-35
13	323	11.8	462	9	TRPE_METTH	ANTHRANILATE SYNTHASE	6.08e-34
14	299	10.9	462	9	TRPE_THETH	ANTHRANILATE SYNTHASE	7.90e-30
15	296	10.8	457	9	TRPE_THEME	ANTHRANILATE SYNTHASE	2.56e-29
16	297	10.8	494	9	TRPE_CLOTM	ANTHRANILATE SYNTHASE	1.73e-29
17	292	10.7	508	9	TRPE_BACCA	ANTHRANILATE SYNTHASE	1.22e-28
18	290	10.6	492	9	TRPE_PSEAE	ANTHRANILATE SYNTHASE	2.66e-28
19	288	10.5	462	9	TRPE_LEPBI	ANTHRANILATE SYNTHASE	5.79e-28
20	279	10.2	493	9	TRPE_PSEPU	ANTHRANILATE SYNTHASE	1.90e-26
21	278	10.2	497	9	TRPE_ACICA	ANTHRANILATE SYNTHASE	2.79e-26
22	280	10.2	505	9	TRPE_PSESS	ANTHRANILATE SYNTHASE	1.29e-26
23	280	10.2	723	7	PABS_STRGR	PARA-AMINOBENZOATE SY	1.29e-26
24	269	9.8	454	7	PABB_SALTY	PARA-AMINOBENZOATE SY	8.91e-25
25	264	9.6	475	7	PABB_STRLI	PARA-AMINOBENZOATE SY	6.04e-24
26	260	9.5	482	9	TRPE_SPIAU	ANTHRANILATE SYNTHASE	2.78e-23
27	261	9.5	506	9	TRPE_YEAST	ANTHRANILATE SYNTHASE	1.90e-23
28	251	9.2	451	7	PABB_KLEAE	PARA-AMINOBENZOATE SY	8.42e-22
29	244	8.9	453	7	PABB_ECOLI	PARA-AMINOBENZOATE SY	1.17e-20
30	221	8.1	621	9	TRPX_ARATH	ANTHRANILATE SYNTHASE	5.89e-17
31	219	8.0	470	7	PABB_LACLA	PARA-AMINOBENZOATE SY	1.22e-16
32	219	8.0	729	9	TRPE_RHIME	ANTHRANILATE SYNTHASE	1.22e-16
33	217	7.9	541	9	TRPE_VIBPA	ANTHRANILATE SYNTHASE	2.53e-16
34	212	7.7	595	9	TRPE_ARATH	ANTHRANILATE SYNTHASE	1.55e-15
35	202	7.4	515	9	TRPE_BUCAP	ANTHRANILATE SYNTHASE	5.61e-14
36	193	7.0	520	9	TRPE_SALTY	ANTHRANILATE SYNTHASE	1.35e-12
37	185	6.8	518	9	TRPE_BRELA	ANTHRANILATE SYNTHASE	2.20e-11
38	182	6.6	520	9	TRPE_ECOLI	ANTHRANILATE SYNTHASE	6.20e-11
39	176	6.4	732	9	TRPE_AZOBR	ANTHRANILATE SYNTHASE	4.83e-10
40	164	6.0	530	7	PHNA_PSEAE	ANTHRANILATE SYNTHASE	2.71e-08
41	155	5.7	518	9	TRPE_HAEIN	ANTHRANILATE SYNTHASE	5.16e-07
42	135	4.9	468	1	ARLY_CANAL	ARGININOSUCCINATE LYA	2.73e-04
43	123	4.5	787	7	PABS_YEAST	PARA-AMINOBENZOATE SY	9.42e-03
44	118	4.3	349	11	YIFC_ECOLI	HYPOTHETICAL 39.6 KD	3.89e-02
45	116	4.2	124	9	TRPE_SYNY3	PROBABLE ANTHRANILATE	6.79e-02



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MPsrch\_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Dec 9 17:28:51 1997; MasPar time 14.87 Seconds  
 771.287 Million cell updates/sec

Tabular output not generated.

Title: >US-08-774-104A-2

Description: (1-397) from US08774104A.pep

Perfect Score: 2738

Sequence: 1 MMTYHETRALAQSDLQQLYA.....ETGLKFEPMRQLLKDYNHVE 397

Scoring table: PAM 150

Gap 11

Searched: 91006 seqs, 28888923 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: pir51

1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3  
 8:unann4 9:unann5 10:unann6 11:unann7 12:unann8  
 13:unann9 14:unann10 15:unenc 16:unrev

Statistics: Mean 48.724; Variance 128.010; scale 0.381

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result	Query					Description	Pred. No.
No.	Score	Match	Length	DB	ID		
1	624	22.8	321	10	S27508	hypothetical protein	1.96e-72
2	621	22.7	476	8	S58229	pchA protein - Pseud	5.65e-72
3	457	16.7	391	2	SYECIK	isochorismate synthase	3.45e-47
4	434	15.9	396	9	A40365	siderophore biosynth	8.89e-44
5	380	13.9	430	9	E64059	isochorismate synthase	7.41e-36
6	372	13.6	523	10	A42301	anthranilate synthase	1.08e-34
7	364	13.3	456	6	S35124	anthranilate synthase	1.55e-33
8	361	13.2	421	16	A40635	anthranilate synthase	4.20e-33

9	360	13.1	470	10	A37854	p-aminobenzoate synt	5.85e-33
10	360	13.1	470	16	S66104	gene pab protein - B	5.85e-33
11	337	12.3	512	6	JH0098	anthranilate synthas	1.18e-29
12	328	12.0	515	2	NNBS1	anthranilate synthas	2.26e-28
13	323	11.8	462	10	A40362	anthranilate synthas	1.16e-27
14	299	10.9	462	8	S03316	anthranilate synthas	2.81e-24
15	296	10.8	457	16	S34746	anthranilate synthas	7.39e-24
16	296	10.8	474	10	B64434	anthranilate synthas	7.39e-24
17	297	10.8	494	10	JX0065	anthranilate synthas	5.36e-24
18	292	10.7	508	6	S19266	anthranilate synthas	2.68e-23
19	290	10.6	492	8	D35114	anthranilate synthas	5.08e-23
20	288	10.5	462	8	B32840	anthranilate synthas	9.65e-23
21	279	10.2	493	8	E35115	anthranilate synthas	1.71e-21
22	278	10.2	497	16	S11891	anthranilate synthas	2.35e-21
23	280	10.2	505	8	A39128	anthranilate synthas	1.24e-21
24	280	10.2	723	10	JN0531	p-aminobenzoic acid	1.24e-21
25	269	9.8	454	6	A31132	p-aminobenzoate synt	4.08e-20
26	264	9.6	475	10	JN0578	p-Aminobenzoic acid	1.98e-19
27	260	9.5	482	8	A39132	anthranilate synthas	6.96e-19
28	261	9.5	507	2	NNBY1	anthranilate synthas	5.08e-19
29	251	9.2	451	6	B31132	p-aminobenzoate synt	1.16e-17
30	244	8.9	453	2	AGEC1	p-aminobenzoate synt	1.02e-16
31	221	8.1	621	6	S27752	anthranilate synthas	1.17e-13
32	221	8.1	621	6	JQ1685	anthranilate synthas	1.17e-13
33	219	8.0	729	8	A30904	anthranilate synthas	2.14e-13
34	212	7.7	595	6	JQ1684	anthranilate synthas	1.75e-12
35	202	7.4	515	2	I40052	anthranilate synthas	3.42e-11
36	193	7.0	520	2	NNEB1T	anthranilate synthas	4.78e-10
37	185	6.8	518	6	B24723	anthranilate synthas	4.85e-09
38	183	6.7	520	6	A39812	anthranilate synthas	8.60e-09
39	182	6.6	520	2	NNEC1	anthranilate synthas	1.15e-08
40	177	6.5	518	6	B48967	anthranilate synthas	4.75e-08
41	164	6.0	530	6	A35116	anthranilate synthas	1.80e-06
42	162	5.9	530	6	E35116	anthranilate synthas	3.13e-06
43	160	5.8	328	9	F64187	p-aminobenzoate synt	5.41e-06
44	155	5.7	518	6	C64121	anthranilate synthas	2.11e-05
45	153	5.6	336	9	I54137	p-aminobenzoate synt	3.61e-05